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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/091,019

DATE: 03/27/2002

TIME: 14:16:45

Input Set : A:\Sequence.txt

Output Set: N:\CRF3\03272002\J091019.raw

3 <110> APPLICANT: Harris, Robert B.  
4 Shen, Jane M.  
5 Shahbaz, Manouchehr M.  
7 <120> TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins  
9 <130> FILE REFERENCE: 41305-270555  
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/091,019  
C--> 11 <141> CURRENT FILING DATE: 2002-03-05  
11 <150> PRIOR APPLICATION NUMBER: US 60/273,418  
12 <151> PRIOR FILING DATE: 2001-03-05  
14 <160> NUMBER OF SEQ ID NOS: 10  
16 <170> SOFTWARE: PatentIn version 3.1  
18 <210> SEQ ID NO: 1  
19 <211> LENGTH: 1391  
20 <212> TYPE: DNA  
21 <213> ORGANISM: Homo sapiens  
23 <400> SEQUENCE: 1  
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26 gtaggtgctc aaaacatcac agcccggatt ggcgagccac tgggtgctgaa gtgtaagggg 120  
28 gcccccaaga aaccacccca gcggtctgaa tggaaactga acacaggccg gacagaagct 180  
30 tggaaggtcc tgtctcccca gggaggaggc ccctgggaca gtgtggctcg tgtccttccc 240  
32 aacggctccc tcttcttccc ggctgtcggg atccaggatg aggggatttt ccggtgccag 300  
34 gcaatgaaca ggaatggaaa ggagaccaag tccaactacc gagtccgtgt ctaccagatt 360  
36 cctgggaagc cagaaattgt agattctgcc tctgaactca cggctggtgt tcccaataag 420  
38 gtggggacat gtgtgtcaga ggaagctac cctgcaggga ctcttagctg gcacttggtat 480  
40 ggaagcccc tgggtgcctaa tgagaaggga gtatctgtga aggaacagac caggagacac 540  
42 cctgagacag ggctcttcac actgcagtcg gagctaattg tgaccccgag ccggggagga 600  
44 gatccccgtc ccaccttctc ctgtagcttc agcccaggcc ttccccgaca ccgggccttg 660  
46 cgcacagccc ccatccagcc ccgtgtctgg gagcctgtgc ctctggagga ggtccaattg 720  
48 gtggtggagc cagaagggtg agcagtagct cctggtggaa ccgtaaccct gacctgtgaa 780  
50 gtccctgccc agccctctcc tcaaattccac tggatgaagg atggtgtgcc ctgcccctt 840  
52 cccccagcc ctgtgctgat cctccctgag atagggcctc aggaccaggg aacctacagc 900  
54 tgtgtggcca ccattccag ccacgggccc caggaaagcc gtgctgtcag catcagcatc 960  
56 atcgaaccag gcgaggaggg gccaaactgca ggctctgtgg gaggatcagg gctgggaact 1020  
58 ctgacctgg ccctggggat cctggggaggc ctggggacag ccgccctgct cattggggtc 1080  
60 atcttgtggc aaaggcggca acgcccagga gaggagagga agggcccaga aaaccaggag 1140  
62 gaagaggagg agcgtgcaga actgaatcag tcggaggaac ctgaggcagg cgagagtagt 1200  
64 actggagggc cttgaggggc ccacagacag atcccatcca tcagctccct tttctttttc 1260  
66 ccttgaactg ttctggcctc agaccaactc tctcctgtat aatctctctc ctgtataacc 1320  
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70 cacatcttgc a 1391  
73 <210> SEQ ID NO: 2  
74 <211> LENGTH: 1020  
75 <212> TYPE: DNA

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76 <213> ORGANISM: Homo sapiens
78 <220> FEATURE:
79 <221> NAME/KEY: CDS
80 <222> LOCATION: (1)..(1020)
81 <223> OTHER INFORMATION:
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86 Met Ala Ala Gly Thr Ala Val Gly Ala Trp Val Leu Val Leu Ser Leu
87 1          5          10          15
89 tgg ggg gca gta gta ggt gct caa aac atc aca gcc cgg att ggc gag      96
90 Trp Gly Ala Val Val Gly Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu
91          20          25          30
93 cca ctg gtg ctg aag tgt aag ggg gcc ccc aag aaa cca ccc cag cgg      144
94 Pro Leu Val Leu Lys Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg
95          35          40          45
97 ctg gaa tgg aaa ctg aac aca ggc cgg aca gaa gct tgg aag gtc ctg      192
98 Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
99          50          55          60
101 tct ccc cag gga gga ggc ccc tgg gac agt gtg gct cgt gtc ctt ccc      240
102 Ser Pro Gln Gly Gly Gly Pro Trp Asp Ser Val Ala Arg Val Leu Pro
103 65          70          75          80
105 aac ggc tcc ctc ttc ctt ccg gct gtc ggg atc cag gat gag ggg att      288
106 Asn Gly Ser Leu Phe Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Ile
107          85          90          95
109 ttc cgg tgc cag gca atg aac agg aat gga aag gag acc aag tcc aac      336
110 Phe Arg Cys Gln Ala Met Asn Arg Asn Gly Lys Glu Thr Lys Ser Asn
111          100          105          110
113 tac cga gtc cgt gtc tac cag att cct ggg aag cca gaa att gta gat      384
114 Tyr Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp
115          115          120          125
117 tct gcc tct gaa ctc acg gct ggt gtt ccc aat aag gtg ggg aca tgt      432
118 Ser Ala Ser Glu Leu Thr Ala Gly Val Pro Asn Lys Val Gly Thr Cys
119          130          135          140
121 gtg tca gag gga agc tac cct gca ggg act ctt agc tgg cac ttg gat      480
122 Val Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp
123 145          150          155          160
125 ggg aag ccc ctg gtg cct aat gag aag gga gta tct gtg aag gaa cag      528
126 Gly Lys Pro Leu Val Pro Asn Glu Lys Gly Val Ser Val Lys Glu Gln
127          165          170          175
129 acc agg aga cac cct gag aca ggg ctc ttc aca ctg cag tcg gag cta      576
130 Thr Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Gln Ser Glu Leu
131          180          185          190
133 atg gtg acc cca gcc cgg gga gga gat ccc cgt ccc acc ttc tcc tgt      624
134 Met Val Thr Pro Ala Arg Gly Gly Asp Pro Arg Pro Thr Phe Ser Cys
135          195          200          205
137 agc ttc agc cca ggc ctt ccc cga cac cgg gcc ttg cgc aca gcc ccc      672
138 Ser Phe Ser Pro Gly Leu Pro Arg His Arg Ala Leu Arg Thr Ala Pro
139          210          215          220
141 atc cag ccc cgt gtc tgg gag cct gtg cct ctg gag gag gtc caa ttg      720

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142 Ile Gln Pro Arg Val Trp Glu Pro Val Pro Leu Glu Glu Val Gln Leu
143 225                230                235                240
145 gtg gtg gag cca gaa ggt gga gca gta gct cct ggt gga acc gta acc      768
146 Val Val Glu Pro Glu Gly Gly Ala Val Ala Pro Gly Gly Thr Val Thr
147                245                250                255
149 ctg acc tgt gaa gtc cct gcc cag ccc tct cct caa atc cac tgg atg      816
150 Leu Thr Cys Glu Val Pro Ala Gln Pro Ser Pro Gln Ile His Trp Met
151                260                265                270
153 aag gat ggt gtg ccc ttg ccc ctt ccc ccc agc cct gtg ctg atc ctc      864
154 Lys Asp Gly Val Pro Leu Pro Leu Pro Pro Ser Pro Val Leu Ile Leu
155                275                280                285
157 cct gag ata ggg cct cag gac cag gga acc tac agc tgt gtg gcc acc      912
158 Pro Glu Ile Gly Pro Gln Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr
159                290                295                300
161 cat tcc agc cac ggg ccc cag gaa agc cgt gct gtc agc atc agc atc      960
162 His Ser Ser His Gly Pro Gln Glu Ser Arg Ala Val Ser Ile Ser Ile
163 305                310                315                320
165 atc gaa cca ggc gag gag ggg cca act gca ggc tct gtg gga gga tca      1008
166 Ile Glu Pro Gly Glu Glu Gly Pro Thr Ala Gly Ser Val Gly Gly Ser
167                325                330                335
169 ggg ctg gtc tag      1020
170 Gly Leu Val
174 <210> SEQ ID NO: 3
175 <211> LENGTH: 339
176 <212> TYPE: PRT
177 <213> ORGANISM: Homo sapiens
179 <400> SEQUENCE: 3
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185 Trp Gly Ala Val Val Gly Ala Gln Asn Ile Thr Ala Arg Ile Gly Glu
186                20                25                30
189 Pro Leu Val Leu Lys Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg
190                35                40                45
193 Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu
194                50                55                60
197 Ser Pro Gln Gly Gly Gly Pro Trp Asp Ser Val Ala Arg Val Leu Pro
198 65                70                75                80
201 Asn Gly Ser Leu Phe Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Ile
202                85                90                95
205 Phe Arg Cys Gln Ala Met Asn Arg Asn Gly Lys Glu Thr Lys Ser Asn
206                100               105               110
209 Tyr Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp
210                115               120               125
213 Ser Ala Ser Glu Leu Thr Ala Gly Val Pro Asn Lys Val Gly Thr Cys
214                130               135               140
217 Val Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp
218 145                150               155               160
221 Gly Lys Pro Leu Val Pro Asn Glu Lys Gly Val Ser Val Lys Glu Gln
222                165               170               175

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Input Set : A:\Sequence.txt

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225 Thr Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Gln Ser Glu Leu  
226 180 185 190  
229 Met Val Thr Pro Ala Arg Gly Gly Asp Pro Arg Pro Thr Phe Ser Cys  
230 195 200 205  
233 Ser Phe Ser Pro Gly Leu Pro Arg His Arg Ala Leu Arg Thr Ala Pro  
234 210 215 220  
237 Ile Gln Pro Arg Val Trp Glu Pro Val Pro Leu Glu Glu Val Gln Leu  
238 225 230 235 240  
241 Val Val Glu Pro Glu Gly Gly Ala Val Ala Pro Gly Gly Thr Val Thr  
242 245 250 255  
245 Leu Thr Cys Glu Val Pro Ala Gln Pro Ser Pro Gln Ile His Trp Met  
246 260 265 270  
249 Lys Asp Gly Val Pro Leu Pro Leu Pro Pro Ser Pro Val Leu Ile Leu  
250 275 280 285  
253 Pro Glu Ile Gly Pro Gln Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr  
254 290 295 300  
257 His Ser Ser His Gly Pro Gln Glu Ser Arg Ala Val Ser Ile Ser Ile  
258 305 310 315 320  
261 Ile Glu Pro Gly Glu Gly Pro Thr Ala Gly Ser Val Gly Gly Ser  
262 325 330 335  
265 Gly Leu Val

269 &lt;210&gt; SEQ ID NO: 4

270 &lt;211&gt; LENGTH: 336

271 &lt;212&gt; TYPE: DNA

272 &lt;213&gt; ORGANISM: Homo sapiens

274 &lt;400&gt; SEQUENCE: 4

275 gctcaaaaca tcacagcccg gattggcgag ccactggtgc tgaagtgtaa gggggccccc 60  
277 aagaaaccac cccagcggct ggaatggaaa ctgaacacag gccggacaga agcttggaag 120  
279 gtcctgtctc cccagggagg aggcccttg gacagtgtgg ctcgtgtcct tcccaacggc 180  
281 tccctcttcc ttccggctgt cgggatccag gatgagggga ttttccggtg ccaggcaatg 240  
283 aacaggaatg gaaaggagac caagtccaac taccgagtcg gtgtctacca gattcctggg 300  
285 aagccagaaa ttgtagattc tgcctctgaa ctcacg 336

288 &lt;210&gt; SEQ ID NO: 5

289 &lt;211&gt; LENGTH: 20

290 &lt;212&gt; TYPE: DNA

291 &lt;213&gt; ORGANISM: Artificial Sequence

293 &lt;220&gt; FEATURE:

294 &lt;223&gt; OTHER INFORMATION: Oligonucleotide primer

296 &lt;400&gt; SEQUENCE: 5

297 aaccatctcg caaataaata

20

300 &lt;210&gt; SEQ ID NO: 6

301 &lt;211&gt; LENGTH: 20

302 &lt;212&gt; TYPE: DNA

303 &lt;213&gt; ORGANISM: Artificial Sequence

305 &lt;220&gt; FEATURE:

306 &lt;223&gt; OTHER INFORMATION: Oligonucleotide primer

308 &lt;400&gt; SEQUENCE: 6

309 acgcacagaa tctagcgctt

20

312 &lt;210&gt; SEQ ID NO: 7

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Input Set : A:\Sequence.txt

Output Set: N:\CRF3\03272002\J091019.raw

313 <211> LENGTH: 20  
314 <212> TYPE: DNA  
315 <213> ORGANISM: Artificial Sequence  
317 <220> FEATURE:  
318 <223> OTHER INFORMATION: Oligonucleotide primer  
320 <400> SEQUENCE: 7  
321 ctcccttctc attaggcacc 20  
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325 <211> LENGTH: 20  
326 <212> TYPE: DNA  
327 <213> ORGANISM: Artificial Sequence  
329 <220> FEATURE:  
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333 tggggacatg tgtgtcagag 20  
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337 <211> LENGTH: 49  
338 <212> TYPE: DNA  
339 <213> ORGANISM: Artificial Sequence  
341 <220> FEATURE:  
342 <223> OTHER INFORMATION: Oligonucleotide primer  
344 <400> SEQUENCE: 9  
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349 <211> LENGTH: 31  
350 <212> TYPE: DNA  
351 <213> ORGANISM: Artificial Sequence  
353 <220> FEATURE:  
354 <223> OTHER INFORMATION: Oligonucleotide primer  
356 <400> SEQUENCE: 10  
357 acgacggaat tccaccacac tggactagt g 31

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/091,019

DATE: 03/27/2002

TIME: 14:16:47

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Output Set: N:\CRF3\03272002\J091019.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date